We claim:

1. An isolated nucleic acid molecule, comprising a single nucleotide polymorphism (SNP) selected from the group consisting of:

(a) a nucleic acid molecule designated SEQ ID NOS: []; and

(b) a nucleic acid molecule that hybridizes to the nucleic acid molecule of (a) or its complement under highly stringent hybridization conditions.

2. An isolated oligonucleotide comprising at least 17 contiguous nucleotides of the nucleotide sequence set forth as SEQ ID NOS: [], or the complement thereof.

3. The isolated oligonucleotide of claim 2, labeled with a detectable marker.

4. A primer pair suitable for use in the polymerase chain reaction (PCR), comprising two oligonucleotides according to claim 2.

5. The primer pair of claim 4, wherein said oligonucleotides are selected from the group consisting of SEQ ID NOS: [] and [], SEQ ID NOS: [] and [], ...and SEQ ID NOS: [] and [].

6. An isolated nucleic acid molecule, comprising a single nucleotide polymorphism (SNP) selected from the group consisting of:

(a) a nucleic acid molecule designated SEQ ID NOS: []; and

(b) a nucleic acid molecule that hybridizes to the nucleic acid molecule of (a) or its complement under highly stringent hybridization conditions.

7. An isolated oligonucleotide comprising at least 17 contiguous nucleotides of the nucleic acid molecule set forth as SEQ ID NOS: [], or the complement thereof.

8. The isolated oligonucleotide of claim 7, labeled with a detectable marker.

9. A primer pair suitable for use in the polymerase chain reaction (PCR), comprising two oligonucleotides according to claim 7.

10. The primer pair of claim 9, wherein said oligonucleotides are selected from the group consisting of SEQ ID NOS: [] and [], SEQ ID NOS: [] and [], ...and SEQ ID NOS: [] and [].

11. A method for detecting a nucleic acid molecule comprising a single nucleotide polymorphism in a sample, comprising contacting said sample containing nucleic acids with one or more oligonucleotides according to claims 2 or 7, wherein said contacting is effected under high stringency hybridization conditions, and identifying a nucleic acid that hybridizes to said oligonucleotide.

12. A method for detecting a nucleic acid molecule comprising a single nucleotide polymorphism in a sample, comprising contacting said sample with the primer pair of claim 4 or 9, amplifying a nucleic acid molecule using polymerase chain reaction, and detecting said amplification.

13. An isolated nucleic acid molecule, comprising a microsatellite sequnce selected from the group consisting of:

(a) a nucleic acid molecule designated SEQ ID NOS: []; and

(b) a nucleic acid molecule that hybridizes to the nucleic acid molecule of (a) or its complement under highly stringent hybridization conditions.

14. An isolated oligonucleotide comprising at least 17 contiguous nucleotides of the nucleic acid molecule set forth as SEQ ID NOS: [], or the complement thereof.

15. The isolated oligonucleotide of claim 14, labeled with a detectable marker.

16. A primer pair suitable for use in the polymerase chain reaction (PCR), comprising two oligonucleotides according to claim 14.

17. The primer pair of claim 16, wherein said oligonucleotides are selected from the group consisting of SEQ ID NOS: [] and [], SEQ ID NOS: [] and [],.and SEQ ID NOS: [] and [].

18. An isolated nucleic acid molecule, comprising a microsatellite sequence selected from the group consisting of:

(a) a nucleic acid molecule designated SEQ ID NOS: []; and

(b) a nucleic acid molecule that hybridizes to the nucleic acid molecule of (a) or its complement under highly stringent hybridization conditions.

19. An isolated oligonucleotide comprising at least 17 contiguous nucleotides of the nucleic acid molecule set forth as SEQ ID NOS: [], or the complement thereof.

20. The isolated oligonucleotide of claim 19, labeled with a detectable marker.

21. A primer pair suitable for use in the polymerase chain reaction (PCR), comprising two oligonucleotides according to claim 19.

22. The primer pair of claim 21, wherein said oligonucleotides are selected from the group consisting of SEQ ID NOS: [] and [], SEQ ID NOS: [] and [], ...and SEQ ID NOS: [] and [].

23. An isolated nucleic acid molecule, comprising a microsatellite sequence selected from the group consisting of:

(a) a nucleic acid molecule designated SEQ ID NOS: []; and

(b) a nucleic acid molecule that hybridizes to the nucleic acid molecule of (a) or its complement under highly stringent hybridization conditions.

24. An isolated oligonucleotide comprising at least 17 contiguous nucleotides of the nucleic acid molecule set forth as SEQ ID NOS: [] to [], or the complement thereof.

25. The isolated oligonucleotide of claim 24, labeled with a detectable marker.

26. A primer pair suitable for use in the polymerase chain reaction (PCR), comprising two oligonucleotides according to claim 24.

27. The primer pair of claim 26, wherein said oligonucleotides are selected from the group consisting of SEQ ID NOS: [] and [], SEQ ID NOS: [] and [], ...and SEQ ID NOS: []-[].

28. An isolated nucleic acid molecule, comprising a microsatellite sequence selected from the group consisting of:

(a) a nucleic acid molecule designated SEQ ID NOS: []; and

(b) a nucleic acid molecule that hybridizes to the nucleic acid molecule of (a) or its complement under highly stringent hybridization conditions.

29. An isolated oligonucleotide comprising at least 17 contiguous nucleotides of the nucleic acid molecule set forth as SEQ ID NOS: [], or the complement thereof.

30. The isolated oligonucleotide of claim 29, labeled with a detectable marker.

31. A primer pair suitable for use in the polymerase chain reaction (PCR), comprising two oligonucleotides according to claim 29.

32. The primer pair of claim 31, wherein said oligonucleotides are selected from the group consisting of SEQ ID NOS: [] and [], SEQ ID NOS: [] and [], and SEQ ID NOS: []-[].

33. An isolated nucleic acid molecule, comprising a microsatellite sequence selected from the group consisting of:

(a) a nucleic acid molecule designated SEQ ID NOS: []; and

(b) a nucleic acid molecule that hybridizes to the nucleic acid molecule of (a) or its complement under highly stringent hybridization conditions.

34. An isolated oligonucleotide comprising at least 17 contiguous nucleotides of the nucleic acid molecule set forth as SEQ ID NOS: [], or the complement thereof.

35. The isolated oligonucleotide of claim 34, labeled with a detectable marker.

36. A primer pair suitable for use in the polymerase chain reaction (PCR), comprising two oligonucleotides according to claim 34.

37. The primer pair of claim 36, wherein said oligonucleotides are selected from the group consisting of SEQ ID NOS: [] and [], SEQ ID NOS: [] and [], and SEQ ID NOS: []-[].

38. A method for detecting a nucleic acid molecule comprising a microsatellite sequence in a sample, comprising contacting said sample containing nucleic acids with one or more oligonucleotides according to claims 14, 19, 24, 29, or 34, wherein said contacting

is effected under high stringency hybridization conditions, and identifying a nucleic acid that hybridizes to said oligonucleotide.

39. A method for detecting a nucleic acid molecule comprising a microsatellite sequence in a sample, comprising contacting said sample with the primer pair of claims 16, 21, 26, 31, or 36, amplifying a nucleic acid molecule using polymerase chain reaction, and detecting said amplification.

40. A method of determining the population of origin of a fish sample comprising the steps of:

(a) providing an origin genotype database comprising a collection of candidate parent genotypes, wherein each of said candidate parent genotypes represents a distinct population of origin; and

(b) comparing a sample genotype to said candidate parent genotypes, wherein a match between said sample genotype and one of said candidate parent genotypes identifies the population of origin of said sample.

41. A method of determining the origin of a fish sample comprising the steps of:

(a) providing an origin genotype database comprising a collection of candidate genotype profiles, wherein each of said candidate genotype profiles represents a distinct population of origin; and

(b) comparing a sample genotype to said candidate genotype profiles, wherein a match between said

sample genotype and one of said candidate genotype profiles identifies the population of origin of said sample.

42. A method of determining the origin of a fish sample comprising the steps of:

(a) providing a parentage genotype database comprising a collection of candidate parent genotypes, wherein each of said candidate parent genotypes represents a distinct origin; and

(b) comparing a sample genotype to said parentage genotype database, wherein a match between said sample genotype and one of said candidate parent genotypes identifies the origin of said sample.

43. The method of claim 42, wherein said parentage genotype database comprises every potential origin genotype.

44. The method of claim 42, wherein said candidate parent genotypes comprise two or more distinct species.

45. The method of claim 42, wherein said sample and candidate parent genotypes belong to the family Salmonidae.

46. The method of claim 42, wherein said sample and candidate parent genotypes belong to the species *Salmo salar*.

47. The method of claim 42, wherein said sample and candidate parent genotypes belong to the genus tilapia.

48. The method of claim 47, wherein said sample and candidate parent genotypes belong to the species *Oreochromis niloticus*.

49. The method of claim 42, further comprising sample and candidate parent genotypes belonging to a species selected from the group consisting of rainbow trout, halibut, seabass and Atlantic cod.

50. The method of claim 42, further comprising the initial steps of:

(a) extracting nucleic acid corresponding to each of said distinct populations of origin ; and

(b) genotyping the extracted nucleic acid with selected genetic markers to obtain said collection of candidate parent genotypes.

51. The method of claim 50, wherein said nucleic acid is extracted from broodstock individuals.

52. The method of claim 50, wherein said genetic markers are selected from the group consisting of single nucleotide polymorphisms (SNPs), microsatellites, restriction length polymorphisms (RFLPs), amplified fragment length polymorphisms (AFLP), random amplified polymorphic DNA (RAPD), mitochondrial DNA.

53. The method of claim 52, wherein said genetic markers comprise SNPs.

54. The method of claim 53, wherein said SNPs comprise SEQ ID NOS: [].

55. The method of claim 53, wherein said SNPs comprise SEQ ID NOS: [].

56. The method of claim 53, further comprising identifying said SNPs by performing an oligonucleotide ligation assay (OLA).

57. The method of claim 53, further comprising identifying said SNPs by performing a hybridization assay.

58. The method of claim 57, wherein said hybridization assay is performed on a DNA chip.

59. The method of claim 42, wherein the absence of said match excludes said candidate genotypes as the origin of said sample.

60. The method of claim 42, further comprising generating a central database capable of storing said population of candidate parent genotypes.

61. The method of claim 42, wherein said central database is capable of instantaneously comparing said sample genotype to said collection of candidate parent genotypes.

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62. The method of claim 61, wherein said central database of candidate parent genotypes is on the accessible through the internet.